

RAW SEQUENCE LISTING

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Application Serial Number: 10/750 323

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/750,323

DATE: 10/19/2004

TIME: 09:18:42

Input Set : N:\CrF3\RULE60\10750323.raw.txt
 Output Set: N:\CRF4\10192004\J750323.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Pulst, Stefan M

7 (ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
8 ATAXIA-2 AND PRODUCTS RELATED THERETO

10 (iii) NUMBER OF SEQUENCES: 19

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
 14 (B) STREET: 119 North Fourth Street
 15 (C) CITY: Minneapolis
 16 (D) STATE: Minnesota
 17 (E) COUNTRY: USA
 18 (F) ZIP: 55401

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk
 22 (B) COMPUTER: IBM PC compatible
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

-> 27 (A) APPLICATION NUMBER: US/10/750,323
 -> 28 (B) FILING DATE: 30-Dec-2003
 -> 33 (C) CLASSIFICATION: 536

-> 30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/727,084
 32 (B) FILING DATE: 08-OCT-1996

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Muetting, Ann M.
 37 (B) REGISTRATION NUMBER: 33,977
 38 (C) REFERENCE/DOCKET NUMBER: 232.00010101

40 (ix) TELECOMMUNICATION INFORMATION:

41 (A) TELEPHONE: 612/305-1220
 42 (B) TELEFAX: 612/305-1228

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 516 base pairs
 50 (B) TYPE: nucleic acid
 51 (C) STRANDEDNESS: both
 52 (D) TOPOLOGY: both

54 (ii) MOLECULE TYPE: DNA (genomic)

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60 TTGGTAGCAA CGGAAACGGC GGCGCGCGT TTCCGCCGG CTCCGGCGG CTCCGGTC	60
62 TCGGGGGCC TCCCCGCCCTTCTCGTCTCC CCTCTCTCCC CCTCGCCAGC CGGGCGCCC	120
64 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGCGCCCG TGCGTCCCCG CGCGTTCG	180

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66	GCGTCTCCTT	GGCGCGCCCG	GCTCCCCGCT	GTCCCCGCC	GGCGTGCAG	CCGGTGTATG	240
68	GGCCCTCAC	CATGTCGCTG	AAGCCCCAGC	AGCAGCAGCA	GCAGCAGCAG	CAACAGCAGC	300
70	AGCAGCAACA	GCAGCAGCAG	CAGCAGCAGC	AGCCGCCGCC	CGCGGCTGCC	AATGTCCGCA	360
72	AGCCCCGG	CAGCGGCCCTT	CTAGCGTCGC	CGCGGCCGCC	GCCTTCGCCG	TCCTCGTCCT	420
74	CGGTCTCCTC	GTCCCTCGGCC	ACGGCTCCCT	CCTCGGTGGT	CGCGGCGACC	TCCGGCGGCC	480
76	GGAGGCCCGG	CCTGGGCAGG	TGGGTGTCGG	CACCCC			516
78	(2) INFORMATION FOR SEQ ID NO: 2:						
80	(i) SEQUENCE CHARACTERISTICS:						
81	(A) LENGTH: 4481 base pairs						
82	(B) TYPE: nucleic acid						
83	(C) STRANDEDNESS: both						
84	(D) TOPOLOGY: both						
86	(ii) MOLECULE TYPE: cDNA						
89	(ix) FEATURE:						
90	(A) NAME/KEY: CDS						
91	(B) LOCATION: 163..4101						
94	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:						
96	ACCCCCGAGA	AAGCAACCCA	GGCGCCGCC	CGCTCCTCAC	GTGTCCCTCC	GGGCCCCGGG	60
98	GCCACCTCAC	GTCTGCTTC	CGTCTGACCC	CTCCGACTTC	CGGTAAAGAG	TCCCTATCCG	120
100	CACCTCCGCT	CCCACCCGGC	GCCTCGGC	GCCCGCCCTC	CG ATG CGC TCA GCG		174
101					Met Arg Ser Ala		
102					1		
104	GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC						222
105	Ala Ala Ala Pro Arg Ser Pro Ala Val Ala Thr Glu Ser Arg Arg Phe						
106	5 10 15 20						
108	GCC GCA GCC AGG TGG CCC GGG TGG CGC TCG CTC CAG CGG CCG GCG CGG						270
109	Ala Ala Ala Arg Trp Pro Gly Trp Arg Ser Leu Gln Arg Pro Ala Arg						
110	25 30 35						
112	CGG AGC GGG CGG GGC GGT GGC GCG GCC CCG GGA CCG TAT CCC TCC						318
113	Arg Ser Gly Arg Gly Gly Gly Ala Ala Pro Gly Pro Tyr Pro Ser						
114	40 45 50						
116	GCC GCC CCT CCC CCG CCC GGC CCC CCT CCC TCC CGG CAG AGC						366
117	Ala Ala Pro Pro Pro Gly Pro Gly Pro Pro Ser Arg Gln Ser						
118	55 60 65						
120	TCG CCT CCC TCC GCC TCA GAC TGT TTT GGT AGC AAC GGC AAC GGC GGC						414
121	Ser Pro Pro Ser Ala Ser Asp Cys Phe Gly Ser Asn Gly Asn Gly						
122	70 75 80						
124	GGC GCG TTT CGG CCC GGC TCC CGG CGG CTC CTT GGT CTC GGC GGG CCT						462
125	Gly Ala Phe Arg Pro Gly Ser Arg Arg Leu Leu Gly Leu Gly Pro						
126	85 90 95 100						
128	CCC CGC CCC TTC GTC GTC GTC CTT CTC CCC CTC GCC AGC CCG GGC GCC						510
129	Pro Arg Pro Phe Val Val Val Leu Leu Pro Leu Ala Ser Pro Gly Ala						
130	105 110 115						
132	CCT CCG GCC GCG CCA ACC CGC GCC TCC CCG CTC GGC GCC CGT GCG TCC						558
133	Pro Pro Ala Ala Pro Thr Arg Ala Ser Pro Leu Gly Ala Arg Ala Ser						
134	120 125 130						
136	CCG CCG CGT TCC GGC GTC TCC TTG GCG CGC CCG GCT CCC GGC TGT CCC						606
137	Pro Pro Arg Ser Gly Val Ser Leu Ala Arg Pro Gly Cys Pro						
138	135 140 145						

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140	CGC CCG GCG TGC GAG CCG GTG TAT GGG CCC CTC ACC ATG TCG CTG AAG	654
141	Arg Pro Ala Cys Glu Pro Val Tyr Gly Pro Leu Thr Met Ser Leu Lys	
142	150 155 160	
144	CCC CAG CAG CAG CAG CAG CAG CAA CAG CAG CAG CAA CAG	702
145	Pro Gln	
146	165 170 175 180	
148	CAG CAG CAG CAG CAG CAG CCG CCC GCG GCT GCC AAT GTC CGC	750
149	Gln Gln Gln Gln Gln Pro Pro Ala Ala Ala Asn Val Arg	
150	185 190 195	
152	AAG CCC GGC GGC AGC GGC CTT CTA GCG TCG CCC GCC GCG CCT TCG	798
153	Lys Pro Gly Gly Ser Gly Leu Leu Ala Ser Pro Ala Ala Ala Pro Ser	
154	200 205 210	
156	CCG TCC TCG TCC TCG GTC TCC TCG TCC GCC ACG GCT CCC TCC TCG	846
157	Pro Ser Ser Ser Val Ser Ser Ser Ala Thr Ala Pro Ser Ser	
158	215 220 225	
160	GTG GTC GCG GCG ACC TCC GGC GGG AGG CCC GGC CTG GGC AGA GGT	894
161	Val Val Ala Ala Thr Ser Gly Gly Arg Pro Gly Leu Gly Arg Gly	
162	230 235 240	
164	CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA	942
165	Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly	
166	245 250 255 260	
168	ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC	990
169	Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly	
170	265 270 275	
172	TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT	1038
173	Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val	
174	280 285 290	
176	TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT	1086
177	Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His	
178	295 300 305	
180	GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG	1134
181	Glu Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met	
182	310 315 320	
184	GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA	1182
185	Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys	
186	325 330 335 340	
188	GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT	1230
189	Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala	
190	345 350 355	
192	ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC	1278
193	Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro	
194	360 365 370	
196	TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA	1326
197	Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu	
198	375 380 385	
200	AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT	1374
201	Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn	
202	390 395 400	
204	GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG	1422

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205	Glu	Glu	Asn	Tyr	Gly	Val	Val	Ser	Thr	Tyr	Asp	Ser	Ser	Leu	Ser	Ser	
206	405					410					415					420	
208	TAT	ACA	GTG	CCC	TTA	GAA	AGA	GAT	AAC	TCA	GAA	GAA	TTT	TTA	AAA	CGG	1470
209	Tyr	Thr	Val	Pro	Leu	Glu	Arg	Asp	Asn	Ser	Glu	Glu	Phe	Leu	Lys	Arg	
210						425					430					435	
212	GAA	GCA	AGG	GCA	AAC	CAG	TTA	GCA	GAA	GAA	ATT	GAG	TCA	AGT	GCC	CAG	1518
213	Glu	Ala	Arg	Ala	Asn	Gln	Leu	Ala	Glu	Glu	Ile	Glu	Ser	Ser	Ala	Gln	
214						440					445					450	
216	TAC	AAA	GCT	CGA	GTG	GCC	CTG	GAA	AAT	GAT	GAT	AGG	AGT	GAG	GAA	GAA	1566
217	Tyr	Lys	Ala	Arg	Val	Ala	Leu	Glu	Asn	Asp	Asp	Arg	Ser	Glu	Glu	Glu	
218						455					460					465	
220	AAA	TAC	ACA	GCA	GTT	CAG	AGA	AAT	TCC	AGT	GAA	CGT	GAG	GGG	CAC	AGC	1614
221	Lys	Tyr	Thr	Ala	Val	Gln	Arg	Asn	Ser	Ser	Glu	Arg	Glu	Gly	His	Ser	
222						470					475					480	
224	ATA	AAC	ACT	AGG	GAA	AAT	AAA	TAT	ATT	CCT	CCT	GGA	CAA	AGA	AAT	AGA	1662
225	Ile	Asn	Thr	Arg	Glu	Asn	Lys	Tyr	Ile	Pro	Pro	Gly	Gln	Arg	Asn	Arg	
226						485					490					495	500
228	GAA	GTC	ATA	TCC	TGG	GGA	AGT	GGG	AGA	CAG	AAT	TCA	CCG	CGT	ATG	GGC	1710
229	Glu	Val	Ile	Ser	Trp	Gly	Ser	Gly	Arg	Gln	Asn	Ser	Pro	Arg	Met	Gly	
230						505					510					515	
232	CAG	CCT	GGA	TCG	GGC	TCC	ATG	CCA	TCA	AGA	TCC	ACT	TCT	CAC	ACT	TCA	1758
233	Gln	Pro	Gly	Ser	Gly	Ser	Met	Pro	Ser	Arg	Ser	Thr	Ser	His	Thr	Ser	
234						520					525					530	
236	GAT	TTC	AAC	CCG	AAT	TCT	GGT	TCA	GAC	CAA	AGA	GTA	GTT	AAT	GGA	GGT	1806
237	Asp	Phe	Asn	Pro	Asn	Ser	Gly	Ser	Asp	Gln	Arg	Val	Val	Asn	Gly	Gly	
238						535					540					545	
240	GTT	CCC	TGG	CCA	TCG	CCT	TGC	CCA	TCT	CCT	TCC	TCT	CGC	CCA	CCT	TCT	1854
241	Val	Pro	Trp	Pro	Ser	Pro	Cys	Pro	Ser	Pro	Ser	Ser	Arg	Pro	Pro	Ser	
242						550					555					560	
244	CGC	TAC	CAG	TCA	GGT	CCC	AAC	TCT	CTT	CCA	CCT	CGG	GCA	GCC	ACC	CCT	1902
245	Arg	Tyr	Gln	Ser	Gly	Pro	Asn	Ser	Leu	Pro	Pro	Arg	Ala	Ala	Thr	Pro	
246						565					570					575	580
248	ACA	CGG	CCG	CCC	TCC	AGG	CCC	CCC	TCG	CGG	CCA	TCC	AGA	CCC	CCG	TCT	1950
249	Thr	Arg	Pro	Pro	Ser	Arg	Pro	Pro	Ser	Arg	Pro	Ser	Arg	Pro	Pro	Ser	
250						585					590					595	
252	CAC	CCC	TCT	GCT	CAT	GGT	TCT	CCA	GCT	GTC	TCT	ACT	ATG	CCT	AAA		1998
253	His	Pro	Ser	Ala	His	Gly	Ser	Pro	Ala	Pro	Val	Ser	Thr	Met	Pro	Lys	
254						600					605					610	
256	CGC	ATG	TCT	TCA	GAA	GGG	CCT	CCA	AGG	ATG	TCC	CCA	AAG	GCC	CAG	CGA	2046
257	Arg	Met	Ser	Ser	Glu	Gly	Pro	Pro	Arg	Met	Ser	Pro	Lys	Ala	Gln	Arg	
258						615					620					625	
260	CAT	CCT	CGA	AAT	CAC	AGA	GTT	TCT	GCT	GGG	AGG	GGT	TCC	ATA	TCC	AGT	2094
261	His	Pro	Arg	Asn	His	Arg	Val	Ser	Ala	Gly	Arg	Gly	Ser	Ile	Ser	Ser	
262						630					635					640	
264	GGC	CTA	GAA	TTT	GTA	TCC	CAC	AAC	CCA	CCC	AGT	GAA	GCA	GCT	ACT	CCT	2142
265	Gly	Leu	Glu	Phe	Val	Ser	His	Asn	Pro	Pro	Ser	Glu	Ala	Ala	Thr	Pro	
266						645					650					655	660
268	CCA	GTA	GCA	AGG	ACC	AGT	CCC	TCG	GGG	GGA	ACG	TGG	TCA	TCA	GTG	GTC	2190
269	Pro	Val	Ala	Arg	Thr	Ser	Pro	Ser	Gly	Gly	Thr	Trp	Ser	Ser	Val	Val	

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270	665	670	675	
272	AGT GGG GTT CCA AGA TTA TCC CCT AAA ACT CAT AGA CCC AGG TCT CCC			2238
273	Ser Gly Val Pro Arg Leu Ser Pro Lys Thr His Arg Pro Arg Ser Pro			
274	680	685	690	
276	AGA CAG AAC AGT ATT GGA AAT ACC CCC AGT GGG CCA GTT CTT GCT TCT			2286
277	Arg Gln Asn Ser Ile Gly Asn Thr Pro Ser Gly Pro Val Leu Ala Ser			
278	695	700	705	
280	CCC CAA GCT GGT ATT ATT CCA ACT GAA GCT GTT GCC ATG CCT ATT CCA			2334
281	Pro Gln Ala Gly Ile Ile Pro Thr Glu Ala Val Ala Met Pro Ile Pro			
282	710	715	720	
284	GCT GCA TCT CCT ACG CCT GCT AGT CCT GCA TCG AAC AGA GCT GTT ACC			2382
285	Ala Ala Ser Pro Thr Pro Ala Ser Pro Ala Ser Asn Arg Ala Val Thr			
286	725	730	735	740
288	CCT TCT AGT GAG GCT AAA GAT TCC AGG CTT CAA GAT CAG AGG CAG AAC			2430
289	Pro Ser Ser Glu Ala Lys Asp Ser Arg Leu Gln Asp Gln Arg Gln Asn			
290	745	750	755	
292	TCT CCT GCA GGG AAT AAA GAA AAT ATT AAA CCC AAT GAA ACA TCA CCT			2478
293	Ser Pro Ala Gly Asn Lys Glu Asn Ile Lys Pro Asn Glu Thr Ser Pro			
294	760	765	770	
296	AGC TTC TCA AAA GCT GAA AAC AAA GGT ATA TCA CCA GTT GTT TCT GAA			2526
297	Ser Phe Ser Lys Ala Glu Asn Lys Gly Ile Ser Pro Val Val Ser Glu			
298	775	780	785	
300	CAT AGA AAA CAG ATT GAT GAT TTA AAG AAA TTT AAG AAT GAT TTT AGG			2574
301	His Arg Lys Gln Ile Asp Asp Leu Lys Lys Phe Lys Asn Asp Phe Arg			
302	790	795	800	
304	TTA CAG CCA AGT TCT ACT TCT GAA TCT ATG GAT CAA CTA CTA AAC AAA			2622
305	Leu Gln Pro Ser Ser Thr Ser Glu Ser Met Asp Gln Leu Leu Asn Lys			
306	805	810	815	820
308	AAT AGA GAG GGA GAA AAA TCA AGA GAT TTG ATC AAA GAC AAA ATT GAA			2670
309	Asn Arg Glu Gly Glu Lys Ser Arg Asp Leu Ile Lys Asp Lys Ile Glu			
310	825	830	835	
312	CCA AGT GCT AAG GAT TCT TTC ATT GAA AAT AGC AGC AGC AAC TGT ACC			2718
313	Pro Ser Ala Lys Asp Ser Phe Ile Glu Asn Ser Ser Asn Cys Thr			
314	840	845	850	
316	AGT GGC AGC AGC AAG CCG AAT AGC CCC AGC ATT TCC CCT TCA ATA CTT			2766
317	Ser Gly Ser Ser Lys Pro Asn Ser Pro Ser Ile Ser Pro Ser Ile Leu			
318	855	860	865	
320	AGT AAC ACG GAG CAC AAG AGG GGA CCT GAG GTC ACT TCC CAA GGG GTT			2814
321	Ser Asn Thr Glu His Lys Arg Gly Pro Glu Val Thr Ser Gln Gly Val			
322	870	875	880	
324	CAG ACT TCC AGC CCA GCA TGT AAA CAA GAG AAA GAC GAT AAG GAA GAG			2862
325	Gln Thr Ser Ser Pro Ala Cys Lys Gln Glu Lys Asp Asp Lys Glu Glu			
326	885	890	895	900
328	AAG AAA GAC GCA GCT GAG CAA GTT AGG AAA TCA ACA TTG AAT CCC AAT			2910
329	Lys Lys Asp Ala Ala Glu Gln Val Arg Lys Ser Thr Leu Asn Pro Asn			
330	905	910	915	
332	GCA AAG GAG TTC AAC CCA CGT TCC TTC TCT CAG CCA AAG CCT TCT ACT			2958
333	Ala Lys Glu Phe Asn Pro Arg Ser Phe Ser Gln Pro Lys Pro Ser Thr			
334	920	925	930	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10750323.raw.txt
Output Set: N:\CRF4\10192004\J750323.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:30 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:33 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)